

10/587,995

## Sequence Alignment

ABP69565  
ID ABP69565 standard; protein; 704 AA.  
XX  
AC ABP69565;  
XX  
DT 15-JUN-2007 (revised)  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1612.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic; BOND\_PC; axotrophin;  
KW membrane-associated RING-CH protein VII; axotrophin [Homo sapiens];  
KW MARCH7; AXO; MARCH-VII; DKFZP586F1122; AXOT; RNF177;  
KW membrane-associated ring finger (C3HC4) 7, isoform CRA\_a;  
KW membrane-associated ring finger (C3HC4) 7, isoform CRA\_a [Homo sapiens];  
KW unknown; unknown [Homo sapiens];  
KW membrane-associated ring finger (C3HC4) 7;  
KW Membrane-associated ring finger (C3HC4) 7 [Homo sapiens];  
KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5515;  
KW GO6512; GO8270; GO16874; GO46872; GO4842; GO6378.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US005095.  
XX  
PR 05-MAR-2001; 2001US-00799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI; 2002-759812/82.  
DR N-PSDB; ABZ11782.  
DR PC:NCBI; gil2383066.  
DR PC:SWISSPROT; Q9H992.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
PT or coagulation disorders.

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PS Claim 9; SEQ ID NO 1612; 1012pp + Sequence Listing; English.

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CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-  
CC ABZ12066) or their mature protein coding portion, active domain coding  
CC protein or complementary sequences. The polynucleotides are useful for  
CC identifying expressed genes or for physical mapping of human genome. The  
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
CC markers, as a food supplement, for generating antibodies, in medical  
CC imaging, screening and diagnostic assays and for treating cell-  
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
CC arthritis, etc. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
CC information from BOND.

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SQ Sequence 704 AA;

Query Match 100.0%; Score 3584; DB 5; Length 704;  
Best Local Similarity 100.0%; Pred. No. 3.5e-269;  
Matches 704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESKPSRIPRRISVQPSSLSARMMSGSRGSSLNDTYHSRDSSFRLDSEYQSTSASASAS 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MESKPSRIPRRISVQPSSLSARMMSGSRGSSLNDTYHSRDSSFRLDSEYQSTSASASAS 60

Qy 61 PFQSAWYSESEITQGARSRSQNQQRDHDSKRPKLSCTNCTSAGRNVGNGLNTLSDSSWR 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 PFQSAWYSESEITQGARSRSQNQQRDHDSKRPKLSCTNCTSAGRNVGNGLNTLSDSSWR 120

Qy 121 HSQVPRSSSMVLGSFGTDLRERRDSSISNLMDYSHRSGDFTTSSYVQDRVPSY 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 HSQVPRSSSMVLGSFGTDLRERRDSSISNLMDYSHRSGDFTTSSYVQDRVPSY 180

Qy 181 SQGARPKENSMSTLQLNTSSTNHQLPSEHQTILSSRDSRNSLRSNFSSRESESSRSNTQP 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SQGARPKENSMSTLQLNTSSTNHQLPSEHQTILSSRDSRNSLRSNFSSRESESSRSNTQP 240

Qy 241 GFSYSSSRDEAPIISNSERVVSSQRPFQESSDNEGRRTTRRLLSRIASSMSSTFFSRRSS 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 GFSYSSSRDEAPIISNSERVVSSQRPFQESSDNEGRRTTRRLLSRIASSMSSTFFSRRSS 300

Qy 301 QDSLNTRSLNSENSYVSPRILTASQSRSNVPSASEVPDNRASEASQGFRFLRRRWGLSSL 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 QDSLNTRSLNSENSYVSPRILTASQSRSNVPSASEVPDNRASEASQGFRFLRRRWGLSSL 360

Qy 361 SHNHSSESDSENFNQESEGRNTGPWLSSSLRNRCTPLFSRRRREGREDESSRIPTSDTSSR 420  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 361 SHNHSSESDSENFNQESEGRNTGPWLSSSLRNRCTPLFSRRRREGREDESSRIPTSDTSSR 420

Qy 421 SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSSATGGSTSDSAQGGRNTGISGILP 480  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 421 SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSSATGGSTSDSAQGGRNTGISGILP 480

Qy 481 GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDTKSAPS RDPERLQKIKESLL 540  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 481 GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDTKSAPS RDPERLQKIKESLL 540

Qy 541 LEDSEEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKWLQAKINSGSSLEA 600  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 541 LEDSEEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKWLQAKINSGSSLEA 600

Qy 601 VTTCELCKEKLELNLEDFDIHELHRAHANEQAELYEFISSGLYLVVLLHLCEQSFSDMMGN 660  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 601 VTTCELCKEKLELNLEDFDIHELHRAHANEQAELYEFISSGLYLVVLLHLCEQSFSDMMGN 660

Qy 661 TNEPSTRVRFINLARTLQAHMEDLETSEDDSEEDGDHNRTFDIA 704  
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Db 661 TNEPSTRVRFINLARTLQAHMEDLETSEDDSEEDGDHNRTFDIA 704